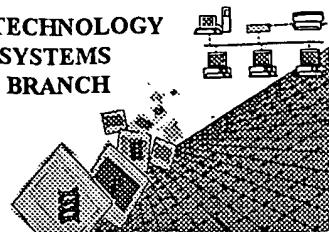


BIOTECHNOLOGY  
SYSTEMS  
BRANCH



**RAW SEQUENCE LISTING**  
**ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/019,596

Source: pus/10

Date Processed by STIC: 8/14/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER** **VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 10/019,596

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
    <210> sequence id number  
    <400> sequence id number  
    000
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
    In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>      Sequence(s) 2 missing the <220> "Feature" and associated numeric identifiers and responses.  
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

1



PCT10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/019,596

DATE: 08/14/2002

TIME: 09:21:24

Input Set : A:\D2398pct\_seq list from client\_30-10-00.txt

Output Set: N:\CRF3\08142002\J019596.raw

Does Not Comply  
Corrected Diskette Needed

pp 1-3

3 <110> APPLICANT: University of Zurich  
5 <120> TITLE OF INVENTION: Hetero-associating coiled coil peptides  
7 <130> FILE REFERENCE: D 2398 PCT  
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/019,596  
C--> 10 <141> CURRENT FILING DATE: 2002-07-11  
12 <160> NUMBER OF SEQ ID NOS: 36  
14 <170> SOFTWARE: PatentIn version 3.0

ERRORED SEQUENCES

714 <210> SEQ ID NO: 36  
715 <211> LENGTH: 37  
716 <212> TYPE: PRT  
717 <213> ORGANISM: artificial sequence  
719 <220> FEATURE:  
720 <221> NAME/KEY: PEPTIDE  
721 <222> LOCATION: (1)..(37)  
722 <223> OTHER INFORMATION: N-acetylated and C-amidated synthetic peptide  
725 <400> SEQUENCE: 36  
727 Ser Thr Ser Val Asp Glu Leu Gln Ala Glu Val Asp Gln Leu Gln Asp  
728 1 5 10 15  
730 Glu Asn Tyr Ala Leu Lys Thr Lys Val Ala Gln Leu Arg Lys Lys Val  
731 20 25 30  
733 Glu Lys Leu Ser Glu  
734 35  
E--> 739 12

delete

see p. 2 for more errors

2



PCT10

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/019,596

DATE: 08/21/2002  
TIME: 20:20:57

Input Set : A:\PTO.AMC.txt  
Output Set: N:\CRF4\08212002\J019596.raw

4 <110> APPLICANT: University of Zurich  
6 <120> TITLE OF INVENTION: Hetero-associating coiled coil peptides  
8 <130> FILE REFERENCE: D 2398 PCT  
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/019,596  
C--> 11 <141> CURRENT FILING DATE: 2002-07-11  
13 <160> NUMBER OF SEQ ID NOS: 36  
15 <170> SOFTWARE: PatentIn version 3.0  
17 <210> SEQ ID NO: 1  
18 <211> LENGTH: 32  
19 <212> TYPE: PRT  
20 <213> ORGANISM: Artificial Sequence  
22 <220> FEATURE:  
23 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic  
24 construct  
26 <220> FEATURE:  
27 <223> OTHER INFORMATION: xaa at positions 5, 7, 12, 14, 19, 21, 26 and  
28 28=mix of glu, lys, gln, arg  
30 <220> FEATURE:  
31 <223> OTHER INFORMATION: xaa at position 15=mix of asn, val  
33 <220> FEATURE:  
34 <221> NAME/KEY: PEPTIDE  
35 <222> LOCATION: (1)..(32)  
39 <400> SEQUENCE: 1

Does Not Comply  
Corrected Diskette Needed

W--> 40 Val Ala Gln Leu Xaa Glu Xaa Val Lys Thr Leu Xaa Ala Xaa Xaa Tyr  
41 1 5 10 15  
W--> 43 Glu Leu Xaa Ser Xaa Val Gln Arg Leu Xaa Glu Xaa Val Ala Gln Leu  
44 20 25 30

49 <210> SEQ ID NO: 2  
50 <211> LENGTH: 32  
51 <212> TYPE: PRT  
52 <213> ORGANISM: Artificial Sequence  
54 <220> FEATURE:

55 <221> NAME/KEY: PEPTIDE  
56 <222> LOCATION: (1)..(32)  
58 <220> FEATURE:

59 <223> OTHER INFORMATION: xaa at positions 5, 7, 12, 14, 19, 21, 26 and  
60 28=mix of glu, lys, gln, arg  
62 <220> FEATURE:  
63 <223> OTHER INFORMATION: xaa at position 15=mix of asn, val  
66 <400> SEQUENCE: 2

W--> 67 Val Asp Glu Leu Xaa Ala Xaa Val Asp Gln Leu Xaa Asp Xaa Xaa Tyr  
68 1 5 10 15  
W--> 70 Ala Leu Xaa Thr Xaa Val Ala Gln Leu Xaa Lys Xaa Val Glu Lys Leu

do you mean

Xaa can be Glu, Lys,  
Gln, or  
Arg?

see item 11 on  
Erra Summary Sheet

Xaa can  
only  
represent  
a single  
distinct  
amino  
acid

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/019,596

DATE: 08/21/2002  
TIME: 20:20:58

Input Set : A:\PTO.AMC.txt  
Output Set: N:\CRF4\08212002\J019596.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 5,7,12,14,15,19,21,26,28  
Seq#:2; Xaa Pos. 5,7,12,14,15,19,21,26,28  
Seq#:25; N Pos. 17,18,19,23,24,25,38,39,40,44,45,46,47,48,49,59,60,61,65,66  
Seq#:25; N Pos. 67,79,80,81,85,86,87  
Seq#:26; Xaa Pos. 5,7,12,14,15,19,21,26,28  
Seq#:27; N Pos. 17,18,19,23,24,25,38,39,40,44,45,46,47,48,49,59,60,61,65,66  
Seq#:27; N Pos. 67,79,80,81,85,86,87  
Seq#:28; Xaa Pos. 5,7,12,14,15,19,21,26,28